

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 17:13:47 ; Search time 17398.4 Seconds
(without alignments)
1042.620 Million cell updates/sec

Title: US-09-303-518D-125
Perfect score: 1344
Sequence: 1 atgattataatcaaaaagg.....ccattgagaagaagctga 1344

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_esttc:*
9: gb_estil:*
10: gb_estst:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	107	8.0	349	12	CNS07GYI
2	39	2.9	684	10	BI728886
3	38.8	2.9	686	9	AL628099
4	38.6	2.9	497	12	P947R
5	38.2	2.8	455	10	BI956450
6	37.8	2.8	437	10	T44736
7	37.6	2.8	384	9	AL392198
8	37.6	2.8	528	10	RG606950
9	37.6	2.8	540	10	BF260729
10	37.6	2.8	544	10	BF260723
11	37.6	2.8	551	10	BF253989
12	37.6	2.8	574	10	BF253938
13	37.6	2.8	622	10	BI957371
14	37.6	2.8	634	10	BI959896
15	37.6	2.8	636	10	BI959473
16	37.6	2.8	697	10	BF628426
17	37.6	2.8	704	10	BF628632

18	37.6	2.8	759	10	BF259476
19	37.6	2.8	764	10	BF616515
20	37.6	2.8	783	10	BF626740
21	37.6	2.8	841	10	BF254527
22	37.6	2.8	847	10	BI957008
23	37.6	2.8	864	10	BI957786
24	37.6	2.8	888	9	AW983120
25	37.2	2.8	376	10	BF293584
26	37.2	2.8	383	10	BF325009
27	37.2	2.8	893	9	AL523270
28	36.8	2.7	481	10	T43876
c	36.6	2.7	458	9	AW1714071
30	36.4	2.7	617	12	AZ935303
c	36.4	2.7	967	12	CNS02UAR
32	36.2	2.7	328	10	BE424405
c	36.2	2.7	407	9	AW12028
34	36.2	2.7	407	10	BF428970
35	36.2	2.7	407	10	BF428970
36	36.2	2.7	460	10	BG262553
37	36.2	2.7	460	10	BE590713
c	36.2	2.7	505	9	AA614629
38	36.2	2.7	595	10	BI479848
39	36.2	2.7	625	10	BE590921
40	36.2	2.7	639	10	BE590517
41	36.2	2.7	943	9	AL556080
42	36	2.7	489	9	AV939450
c	36	2.7	612	12	AQ161443
44	36	2.7	779	10	BI464724
45	35.8	2.7	574	10	BI949252
46	35.8	2.7	621	10	BM490565
47	35.8	2.7	723	12	AQ858218
48	35.6	2.6	320	9	AV938950
49	35.6	2.6	577	9	AV938949
50	35.6	2.6	841	10	BG342965
51	35.4	2.6	642	9	AA263267
52	35.2	2.6	458	10	BG322949
53	35.2	2.6	532	10	BG356450
54	35.2	2.6	580	10	BG262171
55	35.2	2.6	600	10	BI990516
56	35.2	2.6	600	10	BI990766
57	35.2	2.6	619	10	BG464488
58	35.2	2.6	619	10	BE285341
59	35.2	2.6	661	10	BI960403
60	35.2	2.6	915	12	CNS004JJ
c	35	2.6	285	10	BE425275
61	35	2.6	323	9	AI368671
c	35	2.6	349	9	AW808629
63	35	2.6	433	9	AW238848
64	35	2.6	473	9	BB856332
c	35	2.6	497	10	BE378302
66	35	2.6	501	10	BE396602
67	35	2.6	525	10	BE407307
68	35	2.6	546	10	W57645
69	35	2.6	554	10	BE792826
70	35	2.6	582	10	BM042302
71	35	2.6	605	10	BI195835
72	35	2.6	605	10	BE907017
73	35	2.6	624	10	BE394122
74	35	2.6	627	10	BE302953
75	35	2.6	636	10	BE255207
76	35	2.6	650	10	BI064475
77	35	2.6	659	10	BE254129
78	35	2.6	666	10	BG299516
79	35	2.6	671	10	BE794312
80	35	2.6	676	10	BM042451
81	35	2.6	683	10	BM06767
82	35	2.6	686	10	BG761861
83	35	2.6	691	10	BG469125
84	35	2.6	721	10	BE299424
85	35	2.6	727	10	BE612759
86	35	2.6	733	10	BG165939
87	35	2.6	762	10	BI161016
88	35	2.6	764	10	BG481496
89	35	2.6	766	9	AL527125
90	35	2.6	766	9	AL527125

91	35	2.6	768	9	AL559560	AL559560	AL559560
92	35	2.6	772	10	BG760541	BG760541	602718979
93	35	2.6	775	10	BG397732	BG397732	602438793
94	35	2.6	777	10	BG470987	BG470987	602511964
95	35	2.6	779	9	AL538949	AL538949	AL538949
96	35	2.6	779	10	BG575348	BG575348	602597819
97	35	2.6	779	10	BG756437	BG756437	602715767
98	35	2.6	787	9	AL558662	AL558662	AL558662
99	35	2.6	793	10	BG473919	BG473919	602516384
100	35	2.6	793	10	BG743980	BG743980	602722752

ALIGNMENTS

RESULT	1
CNS07GY1	
LOCUS	349 bp DNA linear GSS 02-OCT-2001
DEFINITION	Anopheles gambiae GSS T7 end of clone 23104 of library NotreDame1 from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
ACCESSION	AL610380
VERSION	AL610380.1 GI:15916565
KEYWORDS	GSS.
SOURCE	African malaria mosquito.
ORGANISM	Anopheles gambiae
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
REFERENCE	1 (bases 1 to 349)

REFERENCE	1 (bases 1 to 349)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
REFERENCE	2 (bases 1 to 349)
AUTHORS	Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.
TITLE	Direct Submission
JOURNAL	Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
COMMENT	This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES	Location/Qualifiers			
source	1..349			
	/organism="Anopheles gambiae"			
	/strain="PEST"			
	/db_xref="taxon:7165"			
	/clone="23L04"			
	/clone_lib="NotreDamel"			
	/note="end : T7"			
BASE COUNT	72 a	100 c	106 g	71 t
ORIGIN				
Query Match	8.0%;	Score 107;	DB 12;	Length 349;
Best Local Similarity	58.7%;	Pred. No. 3.6e-19;		
105. Consensitive	0:	Mismatches 130:	Indels 0:	Gaps 0:

Qy	629	atgaattcgccggccgcgcatcttcgcggttttagtggcacacattcattcaatcagc	688
Dd	32	ATGAGTTTGTGGCCCGCATCCGGGGGTCTGTCGGGACGCACATCCATTCTCCTGAGC	91
Qy	689	cggtcgycgcggaataaaacogtgtggaccatcaatatcaagatgttaattaccattggcc	748
Dd	92	CGGTGAGCCTGACAAAACAGGCTGGCATCTTAATTATCAGGAGTGTCATCGCCATCGGTA	151
Qy	749	gtttgtttgcaaacggccgtctgaaacacogacgcgtgatggcctcctagggtgttctcaag	808
Dd	152	CGCTCTTTTCATCATCGGAGAGCTGTGGCGGGAACGGATCATCGCCATCGTGGCGGCCGAGG	211
Qy	809	tcaacaacacgcgccctcttgctacgcgttttaggtgcgaagaataticgcaaatactcggc	868

Db	212	CTGCAACCCGCTGGTGAAGACGCTGATGGCGCGATATCAATGAACCTGCTGAACG	271
QY	869	gcgaattggttgacacagacacacgcgtgattccgggttcggtattgaacgcgcgatta	928
Db	272	AAGAAACCAAGACGAGCGGCAACCGCTGATTCGCGTTCGGTCTCAGTGGCCTGCATG	331
QY	929	cacaaggcgcacg	943
Db	332	CGGTGCAGGCGCACG	346

RESULTS

BI728886	684 bp	mRNA	linear	EST 19-SEP-2001
LOCUS	1031102C06.y1	C. reinhardtii CC-1690, Stress II (normalized), Lambda zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.		
DEFINITION	BI728886			
ACCESSION	BI728886.1	GI:15704597		
VERSION	EST.			
KEYWORDS	Chlamydomonas reinhardtii.			
SOURCE	Chlamydomonas reinhardtii			
ORGANISM	Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonadales.			
REFERENCE	1 (bases 1 to 684)			
AUTHORS	Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C. and Stern, D.			
TITLE	Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analysing Gene Function and Regulation in Vascular Plants. Project: 1031			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Charles Hauser DCMB Box 91000 Duke University Durham, NC 27708-1000 Tel: 919 613 8159 Fax: 919 613 8177 Email: chauser@duke.edu.			
FEATURES	Location/Qualifiers			
source	1..684			

FEATURES
SOURCE

i. 084
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized
), Lambda Zap II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NHA+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Mellis et al., (2000) plant
phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
POLYA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
zap II (Stratagene) in the EcoRI (5') and XhoI (3')
sites. pBluescript II SK- plasmids were excised from the
lambda Zap clones by superinfection with ExAssist
(Stratagene) phage. The library was normalized using
method 4 described in Bonaïdo et al., (1996) Genome
Research 6: 791-806."

	129 a	248 c	203 g	104 t
BASE COUNT				
ORIGIN				

Query Match 2.9%; Score 39; DB 10; Length 684;
 Best Local Similarity 51.4%; Pred. No. 5.9;
 Matches 90; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

	1092	caacacagcgctcaacggcggcgcacgcgcgcattgtgcgataggtaactaccagcgct	1151
Qy			
	1096	CAACACATTCGTAACGGCGCACGCCACGTATGTTGGGGCGGCCTCCGAGGGCCCCAT	255
Db			

Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clmson.edu

Total bp bases = 327
Seq primer: ATTTACCTCTACTAAAGG
High quality sequence stop: 433.
Location/Qualifiers

FEATURES

1. .455
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME003G23f"
/clone_lib="Hordeum vulgare rachis EST library HVCNDA0015 (normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinof's lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinof's A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT
ORIGIN

83 a 150 c 150 g 70 t 2 others

Query Match 2.8%; Score 38.2; DB 10; Length 455;
Best Local Similarity 49.5%; Pred. No. 8.2;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 908 cggattgacgagcgattacacaaagcgagcgagcgattattggagcgctacacaaac 967
|||||
Db 185 CGGTGATCTTCACGCGGAGACGCGGACGCGGCGGCGGCGGCGGCGGCGGCGG 244
QY 968 agatttcggttatcgaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 1027
|||||
Db 245 AGATGAGGCTGCTGACGCTGCGGACGACATCGAGGCTTCGCGGTTGCGACAGA 304
QY 1028 cggacaaatactccatccacgcgtacacccctggcgccattcttgaaaaacaaactctta 1087
|||||
Db 305 TGAGCTCGTACGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 364
QY 1088 agttcaacagccgt 1103
Db 365 AGCCCAAGAGCGCCGT 380

RESULT 6
T44736

LOCUS 7999 Lambda-PRL2 Arabidopsis thaliana cDNA clone 123P217, mRNA
DEFINITION sequence.

ACCESSION T44736
VERSION T44736.1 GI:2759537
KEYWORDS EST.
SOURCE thale cress.

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
1 (bases 1 to 437)
Newman.T., deBruijn.F.J., Green.P., Keegstra.K., Kende.H., McIntosh
.L., Ohlrogge.J., Raikhel.N., Somerville.S., Thomasow.M., Retzel
.E. and Somerville.C.

TITLE

Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729

COMMENT

On Jan 7, 1998 this sequence version replaced gi:949002.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7.

FEATURES

Location/Qualifiers
1. .437
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="123P217"
/clone_lib="Lambda-PRL2"
/note="Vector: lambda zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
silicles). The vector is BRL's lambda zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."

BASE COUNT 99 a 87 c 103 g 132 t 16 others
ORIGIN

Query Match 2.8%; Score 37.8; DB 10; Length 437;
Best Local Similarity 55.8%; Pred. No. 10;
Matches 72; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 128 tgaagtcaaggaaggcgatgccgtcaaaaaagccaaagtgtgttgagacacaaaaaga 187
|||||
Db 71 TCAAAAGCTACACAGATCTCTGAAATCGAAAGCTTGAGCTGTGTATATCGCGGAGAGA 130
QY 188 atccggcggtgtgtttactgcgcgcttcaggcaaaatcgccgagattccaccgtggcg 247
|||||
Db 131 AATGGTGGTATGTGTGACGCGGAGAGCTCCACAGATATCGCGGTGATTAAAGTATTGGG 190
QY 248 aaaaagcgcg 256
Db 191 GAAAGAGAG 199

RESULT 7

AI392198/c

LOCUS AI392198

DEFINITION NCSM1D6T3 Subtracted Mycelial Neurospora crassa cDNA clone SM1D6 5', similar to dolichyl-phosphate-mannose synthase, mRNA sequence.

ACCESSION AI392198

VERSION AI392198.1 GI:4220005

KEYWORDS EST.

SOURCE Neurospora crassa.

ORGANISM Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariales; Sordariaceae; Neurospora.

REFERENCE 1 (bases 1 to 384).

AI392198 384 bp mRNA linear EST 03-FEB-1999
NCSM1D6T3 Subtracted Mycelial Neurospora crassa cDNA clone SM1D6 5', similar to dolichyl-phosphate-mannose synthase, mRNA sequence.

BASE COUNT	ORIGIN	Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/ban/31/cover.html)"
110 a	165 c	174 g 92 t 3 others.

```

BASE COUNT      110 a 165 c 174 g 92 t 3 others.
ORIGIN
Query Match      2.8%  Score 37.6;  DB 10;  Length 544;
Best Local Similarity 49.5%;  pred. No. 13;
Matches 97;  Conservative 0;  Mismatches 99;  Indels 0;  Gaps 0;

QY  908  cgggtattgaacgcgcgattacacaagcgcgacgattatttggagcgtcaccaatc 967
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   167  CGGTGATCTTCAGCGCGGAAGCAGCGGCACGCGCTTCGCGTTCGACAGA 226
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  968  agatttcggttcatcgaagaagggcgacgacaaagcgttgcgtgggttcgcgcgaacg 1027
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   227  AGATGGAGCTCGTCGAGCTCGGCACGACATCAGAGTCTTCGCCAAGGTGGAGCGGGGC 286
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  1028  cggacaataactccatcacgcgtacacccctggccatttcctgaaaaacaaacttca 1087
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   287  TGAGTCTGTACGCGGAGCGCGCAGGAGCGGCCCAAGTCCATCACACCCCTGCTGGAGA 346
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY  1088  agttaacacacgcgct 1103
      || ||| ||| ||| |||
Db   347  AGGCCAAGAGGCGCGT 362
      ||| ||| ||| ||| |||

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RESULT	11
LOCUS	BF253989
DEFINITION	BF253989 551 bp mRNA linear EST 22-OCT-2001 (HVICMF0002L01f Hordeum vulgare seedling root EST library HVCNDA0007 EX10ated and unressed) Hordeum vulgare cDNA clone HVICMF0002L01f, mRNA sequence.
ACCESION	BF253989
VERSION	BF253989.2
KEYWORDS	GI:13116854
SOURCE	barley.
ORGANISM	Hordeum vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Triticeae; Hordeum.
AUTHORS	1 (bases 1 to 551) Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton R.D., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling root cDNA library Unpublished (2001) On Nov 16, 2000 this sequence version replaced gi:11183094. Contact:.....
TITLE	
JOURNAL	
COMMENT	

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FEATURES
source
High quality sequence stop: 540.
Location/Qualifiers
1. .551
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEI0002L01f"
/clone_lib="Hordeum vulgare seedling root EST library
HVCDA0007 (Etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
/notes="Vector: lambdaZAP; site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper

```

RESULT	12
LOCUS	BF265938
DEFINITION	HV_CEA0013L17f Hordeum vulgare seedling green leaf EST library HVCDA0004 Blumeria challenged) Hordeum vulgare cDNA clone HV_CEA0013L17f, mRNA sequence.
ACCESSION	BF265938
VERSION	BF265938.2 GI:13262431
KEYWORDS	EST.
SOURCE	barley.
ORGANISM	Hordeum vulgare
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum. 1 (bases 1 to 574)
AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,X., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi, D.W., Fenton,R.D., Gates,R. and Main,D.
TITLE	Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mial3) seedling leaf cDNA library
JOURNAL	Unpublished (2001)
COMMENT	On Nov 17, 2000 this sequence version replaced gi:11196932. Contact: Wing RA Clemson University Clemson University


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|||||
Db 245 AGATGGAGCTCGTCGAGTCGGCGACGACATCGAGTCTTCCCGCAGGTGGAGCGGGGC 304
QY 1028 cggacaaatactcaccacagcgtacacacccctcgccattctctgaaaaacaaactcttca 1087
Db 305 TGAGCTGTGACGCGCGCGCGAGGAGGCGCGCAAGTCCATCATCACCCCTGTCTGGAGA 364
QY 1088 agttcaacacagccgt 1103
Db 365 AGGCCAAGAGCGCCGT 380

RESULT 14
BI959896
LOCUS
DEFINITION
HVSME0022E12f Hordeum vulgare rachis EST library HVCdNA0015
(normal) Hordeum vulgare cDNA clone HVSME0022E12f, mRNA sequence.
ACCESSION
BI959896
VERSION
BI959896.1 GI:16311151
KEYWORDS
EST.
SOURCE
barley.
ORGANISM
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 634)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons
J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 465
Seq primer: AATTAACCCCTCACTAAAGGG
High quality sequence stop: 605.
Location/Qualifiers
1. 634
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0022E12f"
/clone_lib="Hordeum vulgare rachis EST library HVCdNA0015
(normal)"
/tissue_type="Rachis"
/lab_host="TJCI21"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at Washington State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for

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barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)."
BASE COUNT 131 a 185 c 205 g 113 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 634;
Best Local Similarity 49.5%; Pred. No. 14;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 908 cggattgaacgagcggtattacaaagcgcgacgattattgggagcgtaccacatc 967
|||||
Db 177 CGGTGATCTTCGACGCGCGGAAACGACGCGCGGTTCACGCTCTTCGGTTCACAAGA 236
QY 968 agatttccttattcgaagaagccgcagcaagaagcttctcggttggtcgccgagc 1027
|||||
Db 237 AGATGGAGCTCGTCCACGCTCGCGGACGACATCGAGGTCTTCGCCAAGTGGAGCGGGGC 296
QY 1028 cggacaaatactcaccacagcgtacacacccctcgccattctctgaaaaacaaactctca 1087
|||||
Db 297 TGAGCTCGTACCGCGGAGCGCGGAGGAGCGCGCAAGTCCATCATCACCCCTGTCTGGAGA 356
QY 1088 agttcaacacagccgt 1103
|||||
Db 357 AGGCCAAGAGCGCCGT 372

RESULT 15
BI959473
LOCUS
DEFINITION
BI959473 636 bp mRNA linear EST 22-OCT-2001
HVSME0019N03f Hordeum vulgare rachis EST library HVCdNA0015
(normal) Hordeum vulgare cDNA clone HVSME0019N03f, mRNA sequence.
ACCESSION
BI959473
VERSION
BI959473.1 GI:16310728
KEYWORDS
EST.
SOURCE
barley.
ORGANISM
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 636)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Chin, A., Begum, D.,
Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons
J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 585
Seq primer: AATTAACCCCTCACTAAAGGG
High quality sequence start: 5
High quality sequence stop: 624.
Location/Qualifiers
1. 636
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0019N03f"
/clone_lib="Hordeum vulgare rachis EST library HVCdNA0015
(normal)"
/tissue_type="Rachis"
/lab_host="TJCI21"
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Plants were grown at Washington State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close
lab at the University of California, Riverside total RNA

```

was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

BASE COUNT 132 a 188 c 203 g 113 t
ORIGIN
Query Match 2.8%; Score 37.6; DB 10; Length 636;
Best Local Similarity 49.5%; Pred. No. 14;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 908 cggattgaacgagcgattacacaaagcgagcgacgattattggagcgctaccacaac 967
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 CGGTGATCTTCGACGCGGAGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 234
QY 968 agatttcggtatcgaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 1027
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Db 235 AGATGAGCTGTCGACGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 294
QY 1028 cggacaaatactcatcagcgatcaaacocctggcgacatttcctgaaaaaacaactctca 1087
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 295 TGAGTCGTCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 354
QY 1088 agtcaacacagccgt 1103
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Db 355 AGGCCAAGAGCGCGGT 370

RESULT 16
BF628426 697 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMEB0006A02f Hordeum vulgare seedling shoot EST library
DEFINITION HVCDA0002 (Dehydration stress) Hordeum vulgare cDNA-clone
HVSMEB0006A02f, mRNA sequence.
ACCESSION BF628426
VERSION 1
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 697)
AUTHORS Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, R.D., Oates, R. and Main, D.
TITLE development of a genetically and physically anchored EST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
library

JOURNAL Unpublished (2001)
COMMENT On Dec 19, 2000 this sequence version replaced gi:11892584.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

Total hq bases = 340
Seq primer: AATTAAACCTCACTAAAGG
High quality sequence stop: 681.

FEATURES
source

1..697
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEB0006A02f"
/clone.lib="Hordeum vulgare seedling shoot EST library
HVCDA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJCI21"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 90% RH for 24 hr. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, 600000 pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids.
These steps were performed in the TJ Close laboratory at
the University of California, Riverside (Choi, Close,
Fenton). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)

BASE COUNT 144 a 206 c 220 g 126 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 697;
Best Local Similarity 49.5%; Pred. No. 15;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 908 cggattgaacgagcgattacacaaagcgagcgacgattattggagcgctaccacaac 967
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 169 CGGTGATCTTCGACGCGGAGACGACGCGGCGGCGGCGGCGGCGGCGGCGGCGG 228
QY 968 agatttcggtatcgaagaagcgagcgagcgagcgagcgagcgagcgagcgagcgagc 1027
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Db 229 AGATGAGCTGTCGACGTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 288
QY 1028 cggacaaatactcatcagcgatcaaacocctggcgacatttcctgaaaaaacaactctca 1087
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Db 289 TGAGTCGTCGACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 348
QY 1088 agtcaacacagccgt 1103
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Db 349 AGGCCAAGAGCGCGGT 364

RESULT 17
BF628632 704 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMEB0006N12f Hordeum vulgare seedling shoot EST library
DEFINITION HVCDA0002 (Dehydration stress) Hordeum vulgare cDNA clone
HVSMEB0006N12f, mRNA sequence.
ACCESSION BF628632
VERSION 1
KEYWORDS EST.

SOURCE
ORGANISM

barley.
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

REFERENCE

AUTHORS
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Oates, R. and Main, D.

TITLE

Development of a genetically and physically anchored EST resource
for barley genomics: Morex drought-stressed seedling shoot cDNA
library

JOURNAL

COMMENT
Unpublished (2001)
On Dec 19, 2000 this sequence version replaced gi:11892790.

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293

Email: rwing@clemson.edu

Total hq bases = 580

Seq primer: AATTACCCCTCACTAAAGGG

High quality sequence stop: 663.

FEATURES

Source

1..704
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEb0006N12f"
/clone_lib="Hordeum vulgare seedling shoot EST library
HVCNDA0002 (dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJ121"

/notes="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and ceftaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 90% RH for 24 hr. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, 600000 pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids.
These steps were performed in the TJ Close laboratory at
the University of California, Riverside (Choi, Close,
Fenton). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)"

BASE COUNT
ORIGIN

146 a 206 c 226 g 126 t

Query Match

Best Local Similarity 2.8%; Score 37.6; DB 10; Length 704;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY

908 cggattgaacgagcgattacacagcgccgcacgattatttggagcgctacacatc 967

Db

164 CGGTGATCTTCGACGCGCGGACGCGGCGGTCCAGCTTCCGGTTCGACAAGA 223

QY

968 agatttcgattatcagaagaagcgccgacgaagagctgttcgctgggtgctgcgcgacg 1027

Db 224 AGATGAGTCTCTCGACGTCGGCGAGACATCGAGGTCTTCGCCAAGGTGGAGCGGGC 283
QY 1028 cggacaataactctcatcgcggtacacacccctcgccatttctctgaaaaacaaactctca 1087
Db 284 TGAGTCTGTACGCGGCGCGGCGGAGGAGCGCCCAAGTCCATCACACCCCTGCTGGAGA 343
QY 1088 agttcaacacagccgt 1103
Db 344 AGCCCAAGAGCGCCGT 359

RESULT 18
BF259476

LOCUS

DEFINITION
BF259476 759 bp mRNA linear EST 22-OCT-2001
HVSMEF0019D11f Hordeum vulgare seedling root EST library HVCNDA0007
(Etiolated and unstressed) Hordeum vulgare cDNA clone

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

Location/Qualifiers

1..759

/organism="Hordeum vulgare"

/cultivar="Morex"

/db_xref="taxon:4513"

/clone="HVSMEF0019D11f"

/clone_lib="Hordeum vulgare seedling root EST library
HVCNDA0007 (Etiolated and unstressed)"

/tissue_type="Seedling root"

/lab_host="TJ121"

/note="Vector: lambdaZAP; Site.1: EcoRI; Site.2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and ceftaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see

BASE COUNT
ORIGIN

Query Match	2.8%;	Score 37.6;	DB 10;	Length 764;
Best Local Similarity	49.5%;	Pred. No. 15;		
Matches	97;	Conservative	0;	Mismatches 99;
				Indels 0;
				Gaps 0;

	908	cggattgaacgcgcgattacaagaagcgcgcagattatcttggagcgtatcaccaatt	96
Oy			
	167	CGGTGATCTTCGACGGCGGAAGCAGGCGCGTGCAGCTTCCGTTTGACAAGA	226
Dd			
	nc9	ccatttcggttatcgaagaagccccraccgaagaactattcggttgagttagcgccgacg	102

[illegible][illegible]

Qy	1088	agttcaacacagccgt	1103
Db	347	AGGCCAAGAGCGCGT	362

RESULT	20				
BF626740		783	bp	mRNA	linear
					EST 22-OCT-

LOCUS BF626740 783 bp mRNA linear EST 22-OCT-00

DEFINITION HVSM00001D17f Hordeum vulgare seedling shoot EST library
HVCNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
HVSM00001D17f, mRNA sequence.

ACCESSION BF626740
VERSION BF626740.2 GI:13088174
KEYWORDS EST,

SOURCE
barley.
Hordeum vulgare
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae; Hordeum vulgare.

REFERENCE	1	Triticaceae; Hordeum.
AUTHORS	1 (bases 1 to 783)	Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, I., Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fer, R.D., Oates, R. and Main, D.
TITLE	Development of a genetically and physically anchored EST resource for barley genomics: Morex drought-stressed seedling shoot cDNA library	
JOURNAL	Unpublished (2001)	
COMMENT	On Dec 19, 2000 this sequence version replaced gi:11890904.	

Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 476
Seq primer: AATTAACCCCTCACTAAAGGG
High quality sequence stop: 698.
Location/Qualifiers
1...783

FEATURES
source

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_lib="HVSMB00001D17f"
HVCDA0002 (Hordeum vulgare seedling shoot EST library
/tissue_type="Seedling shoot"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cerotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 90% RH for 24 hr. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, 600000 pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids.
These steps were performed in the TJ Close laboratory at
the University of California, Riverside (Choi, Close,
Fenton). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders/Also
see Close TJ, Wing R, Kleinohs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 177 a 220 c 252 g 134 t
ORIGIN

Query Match 2.8%; Score 37.6; DB 10; Length 783;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 908 cggattgaacgagcgattacacagcgagcgagcatttggagcgatcacacaaac 967
Db 178 CGGTGATCTTCGACCGCGGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 237
QY 968 agatttcggtatcgaagaagcgagcagcagcagcagcagcagcagcagcagc 1027
Db 238 AGATGAGCGTCTGACGTCGCGGAGCAGCGGCGGCGGCGGCGGCGGCGGCGG 11
QY 1028 cggacaaatctccatcacgcgtacacacccctcgccattcttcgaaacaaactctta 1087
Db 298 TGAGCTCGTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 357
QY 1088 agttcaacacagcggt 1103
Db 358 AGGCCAAGAGCGCGGT 373

RESULT 21
BF254527

LOCUS
DEFINITION

BF254527 841 bp mRNA linear EST 22-OCT-2001
HVSMEF0004E12f Hordeum vulgare seedling root EST library HVCDA0007
(Etioiated and unstressed) Hordeum vulgare cDNA clone
HVSMEF0004E12f, mRNA sequence.
BF254527
BF254527.2 GI:13117183
EST.
SOURCE
KEYWORDS
ORGANISM

REFERENCE
AUTHORS

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 841)
Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:11183632.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 416
Seq primer: AATTAACCCCTCACTAAAGGG
High quality sequence stop: 580.
Location/Qualifiers
1..841

TITLE
JOURNAL
COMMENT

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
1 (bases 1 to 841)
Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
On Nov 16, 2000 this sequence version replaced gi:11183632.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 416
Seq primer: AATTAACCCCTCACTAAAGGG
High quality sequence stop: 580.
Location/Qualifiers
1..841

FEATURES
source

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone_lib="HVSMEF0004E12f"
HVCDA0007 (Etioiated and unstressed)
/tissue_type="Seedling root"
/lab_host="TJC121"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cerotaxime in covered
crystallization dishes. Five-day old seedling roots were
then harvested, total RNA was prepared, poly(A) RNA was
purified, one primary unamplified cDNA library was made,
and 1 million pfu were in vivo excised to give pBluescript
SK(-) cDNA phagemids. These steps were performed in the TJ
Close laboratory at the University of California,
Riverside (Choi, Close, Fenton). Phagemids were plated and
picked at the Clemson University Genomics Institute (CUGI)
(Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA
preparations, DNA sequencing and sequence analysis were
performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
, Rambo, Main). The sequence has been trimmed to remove
vector sequence and contains a minimum of 100 bases of
phred value 20 or above. For more details on library
preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders/Also
see Close TJ, Wing R, Kleinohs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT
ORIGIN

192 a 219 c 298 g 132 t

Query Match 2.8%; Score 37.6; DB 10; Length 841;
Best Local Similarity 49.5%; Pred. No. 16;
Matches 97; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

908	cggattgaacgcg	cgattacaagcgcgcacgattatttgggacgtcaccaatc	967
180	CGGTGATCTTCGACGGCAGNAGCACGGGCACGGCTTCCGGTTCCACAAGA	239	
968	agatttcgcttatcgaagaaggccgcagcaagagctgttccgcttggttgcgcgcagc	1027	
240	AGATTGAGCTCGTCGACGCTCGCGGACATCGAGTGCTTCGCCAAGGTGGAGCGCGGGC	299	
1028	cggacaataactcatcagcgtacaaacctcgccatttctgaaaaaacaaactcttoa	1087	
300	TGAGTCGTGATCGCGGACGGCCGACGAGGCGCCCAAGTCCATCATCACCCCTGCTGGAGA	359	
1088	agttaacacacagccgt	1103	
350	AGCCAAGAGCGCGT	375	

RESULT 22
Bi957008
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

      847 bp      mRNA      linear      EST 22-OCT-2001
HVSME0006006f Hordeum vulgare rachis EST library HVCDNA0015
(normal) Hordeum vulgare cDNA clone HVSME0006006f, mRNA sequence.
Bi957008
Bi957008.1 GI:16308261
EST.
barley.
Hordeum vulgare
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Ackins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex rachis cDNA library
Unpublished (2001)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 592
Seq primer: AATTAAACCCTCACTAAAGGG
High quality sequence stop: 667.
Location/Qualifiers
1..847
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0006006f"
/clone_lib="Hordeum vulgare rachis EST library HVCDNA0015
(normal)"
/tissue_type="Rachis"
/lab_host="TJC121"
/notes="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI; Plants were grown at Washington State University,
Pullman, WA in a greenhouse, the rachises were excised and
frozen in liquid nitrogen (Kleinhofs lab). In the TJ Clos
lab at the University of California, Riverside total RNA
was prepared, poly(A) was purified, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Chin). Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The
sequence has been trimmed to remove vector sequence and
contains a minimum of 100 bases of phased value 20 or
above. For more details on library preparation and
```

sequence analysis see
<http://www.genome.clemson.edu/projects/barley/>. To order
 this clone see <http://www.genome.clemson.edu/orders> Also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. *Barley Genetics Newsletter* 31:29-30.
 (<http://wheat.usda.gov/ggpages/bgn/31/cover.html>)
 249, c 258
 249, c 157 t

BASE COUNT
ORIGIN

	Query Match	2.8%;	Score 37.6;	DB 10;	Length 847;
	Best Local Similarity	49.5%;	Pred. No.16;		
	Matches 97;	Conservative	0;	Mismatches	99;
				Indels	0;
				Gaps	0;
QY	908	cggtatigaacgcgcgattacacaagggcgccacgattatttggagcgtaccacaatc	967		
Db	180	CGGTGATCTTCAGCGCGGAACACGGGCACGCGGTTCAGGTTCTCGGTTGCACAAGA	239		
QY	968	agatttcggttatcgaagaagccgcagcaagaagcttccgctgggttcgcccgcgcgc	1027		
Db	240	AGATGGAGCTCGTCAGCTCGGCGAGCATCGAGGTTCTGCCAANGTGGAGCCGGGCG	299		
QY	1028	cggaacaattccatcacgcgtacacacctggccatttccctgaatacaaacattctca	1087		
Db	300	TGAGTCTGTAGCCGGAGCGCCCGCAGGAGCCCAAGTCCATCACACCCCTGCTGGAGA	359		
QY	1088	agttcaacacacgcgt	1103		
Db	360	AGGCCCAAGAGCGCGT	375		

RESULT 23

BI957786	BI957786	864 bp	linear	EST 22-OCT-2001
LOCUS				
DEFINITION	HYSMen0011f07f Hordeum vulgare rachs EST library HVCDNA0015			
ACCESSION	(normal) Hordeum vulgare cDNA clone HVSMen0011f07f, rachs sequence.			
VERSION	BI957786.1			
KEYWORDS	EST.			
SOURCE	Barley.			

REFERENCE AUTHORS	TITLE	JOURNAL
1 (bases 1 to 864) Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D., Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons J., Oates R. and Main,D.	Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library	Unpublished (2001)

COMMENT

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwine@clemson.edu
Total hq bases = 458
Seq primer: AATTAACTCTCACTAAAGG
high quality sequence stop: 641.

FEATURES

```

1. .864
source
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME0011F07f"
/clone_lib="Hordeum vulgare rachis EST library HVCDA0015
(normal)"
/tissue_type="Rachis"
/lab_host="rJc121"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:

```



```

RESULT 26
BF325009      383 bp      mRNA      linear      EST 06-DEC-2001
su18c01.y1 Gm-cl066 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl066-2017 5' similar to TR:Q9SDA7 Q9SDA7 AT2G17030 PROTEIN. ;,
mRNA sequence.
ACCESSION     BF325009.1 GI:11274672
VERSION       BF325009
KEYWORDS      EST.
SOURCE        soybean.
ORGANISM      Glycine max
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Glycine.
REFERENCE     1 (bases 1 to 383)
AUTHORS       Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Coryell,V., Khanna
              ,A., Bolla,B., Marra,M., Hillier,D., Kucaba,T., Martin,J., Beck,C.,
              Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
              ,Y., Person,B., Swaller,T., Gibbons,N., Pape,D., Harvey,N., Schurk
              ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
              ,R., Waterston,R. and Willson,R.
              Public Soybean EST Project
              Unpublished (1999)
              Contact: Shoemaker R/Public Soybean EST Project
              Public Soybean EST Project
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              This clone is available through: ResGen, Invitrogen Corp. 2130
              South Memorial Parkway Huntstville, AL 35801 For further information
              call: (800)-533-4363 or contact via email: ccu@resgen.com
              Insert Length: 1093 Std Error: 0.00
              High quality sequence stop: 382.
FEATURES             Location/Qualifiers
                     1..383
                        /organism="Glycine max"
                        /db_xref="taxon:3847"
                        /clone="GENOME SYSTEMS CLONE ID: Gm-cl066-2017"
                        /clone_lib="Gm-cl066"
                        /tissue_type="leaf and shoot tip, salt stressed, 2 week
                        old seedling"
                        /lab_host="DH10B"
                        /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                        XhoI; The cDNA library was constructed from mRNA isolated
                        from unexpanded leaves and the shoot tips of 2 week old
                        seedling from the cultivar Williams. The 2 week old
                        seedlings were salt stressed in a solution of 500mM NaCl
                        for 3 days prior to harvesting. Complementary DNA was
                        synthesized from mRNA using a primer consisting of a
                        poly(dT) sequence with a XhoI restriction site. EcoRI
                        adapters were ligated to the blunt-ended cDNA fragments
                        followed by XhoI digestion. The cDNA fragments were
                        directionally cloned into the EcoRI-XhoI restriction site
                        of the pBluescript vector. The ligated cDNA fragments were
                        transformed into DH10B host cells.(GibcoBRL). This library
                        was constructed in the laboratory of Dr. Randy
                        Shoemaker."
BASE COUNT      75 a    91 c   137 g   79 t    1 others
ORIGIN
Query Match      2.8%; Score 37.2; DB 10; Length 383;
Best Local Similarity 48.6%; Pred. No. 14;
Matches 102; Conservative 0; Mismatches 108; Indels 0; Gaps 0;
Qy 1083 cttaagattcaacacgccgtacaaggcgagccgcgaatggtagcgattgacttta 1142
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 52 CGTCAGCGTGCGGGCGATGATGCGGTGGCTCACCTTCGCCGCCGAGCGCTGTTGGTGG 111
         ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Ov 1143 caaccgatatagcccttgatatctaccacacctgcttttgccgcgattkaatgctcg 1202

```

BF293584.1 GI:11224648

EST.
Triticum turgidum.
Triticum turgidum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 376)
Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R.,
Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C.
and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Whole plant cDNA library from Triticum turgidum L. var.
durum
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..376
/organism="Triticum turgidum"
/cultivar="Langdon-16"
/db_xref="taxon:4571"
/clone="WHE2158.E09.J18"
/clone_lib="Triticum turgidum L. var. durum (durum wheat)"
whole_plant_cDNA_library
/tissue_type="All tissues"
/dev_stage="Different growth stages"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site.1: EcoRI; Site.2: XhoI; plants were grown in a growth
chamber at North Dakota State University (Kianian, Otto,
Simons). Tissues collected from seven-day etiolated
seedling leaf, stem, root and seed; leaf from plant at
fourth leaf stage; spike from pre-anthesis through 20
days after anthesis; flag leaf; leaf and stem tissue from
tillers, and root. Total RNA and poly(A) RNA were
prepared from each tissue and then pooled, a cDNA library
was made, and the cDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Akhunov, Chin,
Choi, Close, Fenton, Kianian, Otto, Simons, Zhang) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
BASE COUNT 37 a 154 c 136 g . 49 t
ORIGIN

Query Match 2.8%; Score 37.2; DB 10; Length 376;
Best Local Similarity 55.4%; Pred. No. 14;
Matches 72; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 1197 cgctggcgataccacgagcgcaggcatgttggttgtgaattggacgaagacct 1256
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 CGGCGCGAGCCGGCGGCCGGAGGTGCCCTCAGCTGGAGTGCGGTGGAGGACGT 116
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1257 cgctttgtcacgttcgtctgccgcccgaatacgcgccgcgtgtgtgcgcaaat 1316
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 GCCGCAGCAGCGTTTCGCTTCGGGGCGCCGGCGGACGAGGCGGTGCGCGCGGT 176
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1317 gctggaacc 1326
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 GCTGCAGAGC 186
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||


```

Db 112 CGAAGAAGTTCCTCGTGGAGTCCGAGGCGCGTGTGCTGCGACATGTACCTC 171
QY 1203 cgataccagcagcgagcagcattggttggattggaattgacgaagaagacccgttt 1262
Db 172 CTACTACTCTCGTGCAGCAGGTTTGTTCACGAGGATTTCACGAGGAAGATGTGGCCG 231
QY 1263 gtgcagcttctgtcccgaggcaatacga 1292
Db 232 GATGGGCTGGAGAGGACGGTGAAGTTGA 261

RESULT 27
AL523270
LOCUS
DEFINITION
AL523270 LTI_NFL003_NBC3 893 bp mRNA linear EST 13-FEB-2001
prime mRNA sequence.
ACCESSION
AL523270
VERSION
AL523270.1 GI:12786763
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 893)
AUTHORS
Li.W.B., Gruber.C., Jessee.J. and Polayes.D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
source
1. .893
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC001YH12"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
/tissue_type="neuroblastoma cells"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Peng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
BASE COUNT 168 a 282 c 285 g 153 t 5 others
ORIGIN

```

```

Query Match 2.8%; Score 37.2; DB 9; Length 893;
Best Local Similarity 54.8%; Pred. No. 22;
Matches 69; Conservative 2; Mismatches 55; Indels 0; Gaps 0;

QY 1215 cgcgcagcattggttggattggaattgacgaagaagacctcgtttgtgagcttcgt 1274
Db 258 CGGGGCTGCAACGCCAGCKCTCAGGGCCGCCGAGGATGGGCTCGCTGCTGCC 317
QY 1275 ctgccggcgcaatacgaatacggcccgctgtgtgcgaagtgtcggaaccattgagaa 1334
Db 318 CAACCCGGGCACATTCGAGGATGGCACCGGAAGTGAAGGAGCTGTTTCCCATTCAGAT 377
QY 1335 ggaagg 1340
Db 378 GGAGGG 383

```

RESULT 28

```

T43876
LOCUS
DEFINITION
7139 Lambda-PRL2 Arabidopsis thaliana cDNA clone 118M9T7, mRNA
sequence.
ACCESSION
T43876
VERSION
T43876.1 GI:948248
KEYWORDS
EST.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE
1 (bases 1 to 481)
AUTHORS
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel
,E. and Somerville,C.
TITLE
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
COMMENT
On Nov 29, 1993 this sequence version replaced gi:636464.
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@bm.cl.msu.edu
Seq primer: T7
Location/Qualifiers
1. .481
/organism="Arabidopsis thaliana"
/strain="var columbia"
/db_xref="taxon:3702"
/clone="118M9T7"
/clone_lib="Lambda-PRL2"
/notes="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques). The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."
BASE COUNT 122 a 96 c 113 g 133 t 17 others
ORIGIN

```

```

Query Match 2.7%; Score 36.8; DB 10; Length 481;
Best Local Similarity 55.0%; Pred. No. 21;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 128 tgaagtcaaggaaggcgtgcgcgcacaaaggccaaagctgtgttgaagacaaaaga 187
Db 47 TCAAGCTACACAGATCTCTGGAATCGAAAAGCTTGACTGTGTATATGCGGAGGAGA 106
QY 188 atccggcggtgttactgcgcgcgttcaggcaaaatgcgcgcattccacgtggtcg 247
Db 107 AATGGGTGTGTGTGTGAGCGGCAGACTCCAAAGATATCGCGGTGATTAAGTATTGGG 166
QY 248 aaagcgcg 256
Db 167 GAAAGAGAG 175

```

RESULT 29
AW14071/c
LOCUS
DEFINITION

AW14071 458 bp mRNA linear EST 25-APR-2000
h5f02ne.fl Neurospora crassa evening cDNA library Neurospora crassa
cDNA clone h5f02ne 5', mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
Genome Res. 11 (8), 1434-1440 (2001)
21376150
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 560.
Location/Qualifiers
1. .617
/organism="Bradyrhizobium japonicum"
/strain="USDA110"
/db_xref="taxon:375"
/clone_lib="B. japonicum BAC library"
/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: HindIII"
BASE COUNT 108 a 193 c 216 g 98 t 2 others
ORIGIN
Query Match 2.7%; Score 36.4; DB 12; Length 617;
Best Local Similarity 47.9%; Pred. No. 30;
Matches 103; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 1101 cgtcaacggcgagcgccgattggtgcgattggtgtaactacgagcgctgacccctt 1160
Db 328 CATCATGACGGCGGCGGACCATCGGCGGCGTTCGAGGCGCATGAGCGGGCGGT 387
QY 1161 ggtatctgcccacccctgcttttgcgcgatttaactgcgcgataccgacgagcgca 1220
Db 388 CGACTACATTTCTCAAGCCGTTCAAGCTCAGCGTCGCTATCCCGTCTCGAGCGCGGT 447
QY 1221 ggcattgggtgcttggaattgacgaagaagacctcgtttgtgcagcttgcgttcgcc 1280
Db 448 CGGGTGGCGGCGCTGCACCTGGAGATGNGAGCTGGGCTCGGGTCCGCGAGCGGAC 507
QY 1281 gggcaatacgaatacggcgctgtgtgcgcaaa 1315
Db 508 CCTCGAGTCTGAAGCGCCGCCACCGGGAGCTCGAGG 542
RESULT 31
CNS02UAR/c
LOCUS
DEFINITION
CNS02UAR 967 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
166L18 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL214236.1 GI:7873055
VERSION
GSS: genome survey sequence.
KEYWORDS
SOURCE
ORGANISM
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Fizes.C., Fisher.C.,
Bouneau.L., Billault.A., Quetier.F., Saurin.W., Bernot.A. and
Weissenbach.J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Bouneau.L., Fisher.C.,

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
Genome Res. 11 (8), 1434-1440 (2001)
21376150
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 560.
Location/Qualifiers
1. .617
/organism="Bradyrhizobium japonicum"
/strain="USDA110"
/db_xref="taxon:375"
/clone_lib="B. japonicum BAC library"
/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: HindIII"
BASE COUNT 108 a 193 c 216 g 98 t 2 others
ORIGIN
Query Match 2.7%; Score 36.4; DB 12; Length 617;
Best Local Similarity 47.9%; Pred. No. 30;
Matches 103; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 1101 cgtcaacggcgagcgccgattggtgcgattggtgtaactacgagcgctgacccctt 1160
Db 328 CATCATGACGGCGGCGGACCATCGGCGGCGTTCGAGGCGCATGAGCGGGCGGT 387
QY 1161 ggtatctgcccacccctgcttttgcgcgatttaactgcgcgataccgacgagcgca 1220
Db 388 CGACTACATTTCTCAAGCCGTTCAAGCTCAGCGTCGCTATCCCGTCTCGAGCGCGGT 447
QY 1221 ggcattgggtgcttggaattgacgaagaagacctcgtttgtgcagcttgcgttcgcc 1280
Db 448 CGGGTGGCGGCGCTGCACCTGGAGATGNGAGCTGGGCTCGGGTCCGCGAGCGGAC 507
QY 1281 gggcaatacgaatacggcgctgtgtgcgcaaa 1315
Db 508 CCTCGAGTCTGAAGCGCCGCCACCGGGAGCTCGAGG 542
RESULT 31
CNS02UAR/c
LOCUS
DEFINITION
CNS02UAR 967 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
166L18 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL214236.1 GI:7873055
VERSION
GSS: genome survey sequence.
KEYWORDS
SOURCE
ORGANISM
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Fizes.C., Fisher.C.,
Bouneau.L., Billault.A., Quetier.F., Saurin.W., Bernot.A. and
Weissenbach.J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Bouneau.L., Fisher.C.,

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
COMMENT
Genome Res. 11 (8), 1434-1440 (2001)
21376150
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Class: BAC ends
High quality sequence stop: 560.
Location/Qualifiers
1. .617
/organism="Bradyrhizobium japonicum"
/strain="USDA110"
/db_xref="taxon:375"
/clone_lib="B. japonicum BAC library"
/lab_host="E. coli"
/note="Vector: pIndigo536; Site_1: HindIII"
BASE COUNT 108 a 193 c 216 g 98 t 2 others
ORIGIN
Query Match 2.7%; Score 36.4; DB 12; Length 617;
Best Local Similarity 47.9%; Pred. No. 30;
Matches 103; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 1101 cgtcaacggcgagcgccgattggtgcgattggtgtaactacgagcgctgacccctt 1160
Db 328 CATCATGACGGCGGCGGACCATCGGCGGCGTTCGAGGCGCATGAGCGGGCGGT 387
QY 1161 ggtatctgcccacccctgcttttgcgcgatttaactgcgcgataccgacgagcgca 1220
Db 388 CGACTACATTTCTCAAGCCGTTCAAGCTCAGCGTCGCTATCCCGTCTCGAGCGCGGT 447
QY 1221 ggcattgggtgcttggaattgacgaagaagacctcgtttgtgcagcttgcgttcgcc 1280
Db 448 CGGGTGGCGGCGCTGCACCTGGAGATGNGAGCTGGGCTCGGGTCCGCGAGCGGAC 507
QY 1281 gggcaatacgaatacggcgctgtgtgcgcaaa 1315
Db 508 CCTCGAGTCTGAAGCGCCGCCACCGGGAGCTCGAGG 542
RESULT 31
CNS02UAR/c
LOCUS
DEFINITION
CNS02UAR 967 bp DNA linear GSS 15-MAY-2000
Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
166L18 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL214236.1 GI:7873055
VERSION
GSS: genome survey sequence.
KEYWORDS
SOURCE
ORGANISM
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Fizes.C., Fisher.C.,
Bouneau.L., Billault.A., Quetier.F., Saurin.W., Bernot.A. and
Weissenbach.J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Unpublished
2 (bases 1 to 967)
Roest-Crollius.H., Jaillon.O., Dasilva.C., Bouneau.L., Fisher.C.,

```

source
1. 328
/organism="Triticum aestivum"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0078_E09_J18"
/clone_lib="Wheat endosperm cDNA library"
/tissue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/notes="Vector: Lambda ZAP II, excised phagemid: Site_1:
ECORI; Seeds collected, endosperm isolated, and RNA
prepared by Susan Altenbach. Library constructed by
Stratagene, Inc. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab."
96 a 83 c 86 g 66 t
BASE COUNT

```

BASE COUNT	96 a	83 c	83 g	66 t	Query Match	2.7%;	Score 36.2;	DB 10;	Length 328;
ORIGIN	a sequencing was performed in the OD Anderson lab."				Best Local Similarity 50.3%;	Pred. No. 26;	Mismatches 0;	Indels 88;	Gaps 0;
	Matches 89;	Conservative							
QY	152	tcaaaaagcccaagtgcgtgtttgaagacaaaaaataccggcggtgtgtttactgcgc	211						
Db	62	TCAAGCATGGTGTGACAGATCTTTGGACGAAGCAAAACAGGTCTTCTGGACACACAGTGC	121						
QY	212	cggcttcaggcaaaaatccgcgcgattcacctggcgcgaaacgcgacttcagtcagtcg	271						
Db	122	AACTGGCAATCAAAATCTCTGGCATCTACTGGTGTACTAAGGTTCCAAAGCATTCGAGCG	181						
QY	272	tgattgcggttgaaagcaacgcgcgaatactgagtttgaaacgctacgcacctgaagcgc	328						
Db	182	AGGTACAGCTGGGTACTACAATTACATGATAGAGACGGCTACAGACCCATTAGCAC	238						

```

AW712028.1  GI:7601100
EST.
Neurospora crassa.
Neurospora crassa
Eukaryota: Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 407)
Zhu,H., Lal,H., Kupfer,D., Dunlap,J.C. and Roe,B.A.
Two Neurospora crassa EST Databases
Unpublished (1998)
Other ESTs: f7c01ne.r1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 263.
Location/Qualifiers
1. .407
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
/clone_lib="Neurospora"
/clone="f7c01ne"
/tissue="Neurospora crassa evening cDNA library"
/dark_type="tissue harvested following 22hr growth in
dark"
/note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2:

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was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).

BASE COUNT 131 a 117 c 118 g 94 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 30;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 152 tcaaaagggccaaagtctgtttgaagacaaagaaatccggcggtgtttactgcgc 211
DB 191 TCAAGCATGTTGACAGATCTTGGACGACCAACAAAGGCTTCTTTGGACACACAGTGC 250
QY 212 cggcttcaggcaaaatccgcgattccacgtgagaaagcgcgtacttcagtcagtcg 271
DB 251 AACTGGCAATCAAAATCTCTGGCAATCTCACTGGTGTGTTACAAGGTTCCAAAGCCATGACGCG 310
QY 272 tgattgcgtttgaaggaacgcgcgaatcgagtttgaaacgtacgcacctgaagcgc 328
DB 311 AGGTACACAGCTGGTACTACAACTTACATGATAGACGCGCTACAGACCCATAGCAC 367

RESULT 36
BE590713
LOCUS
DEFINITION
WHE0856_A07_A142S Wheat 20-45 DAP spike cDNA library. Triticum aestivum cDNA clone WHE0856_A07_A14, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
1 (bases 1 to 460)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105955773
Fax: 5105959518
Email: andersn@wp.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..460
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0856_A07_A14"
/clone_lib="Wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab

FEATURES
source

(Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).

BASE COUNT 129 a 117 c 114 g 100 t
ORIGIN

Query Match 2.7%; Score 36.2; DB 10; Length 460;
Best Local Similarity 50.3%; Pred. No. 30;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 152 tcaaaagggccaaagtctgtttgaagacaaagaaatccggcggtgtttactgcgc 211
DB 227 TCAAGCATGTTGACAGATCTTGGACGACCAACAAAGGCTTCTTTGGACACACAGTGC 286
QY 212 cggcttcaggcaaaatccgcgattccacgtgagaaagcgcgtacttcagtcagtcg 271
DB 287 AACTGGCAATCAAAATCTCTGGCAATCTCACTGGTGTGTTACAAGGTTCCAAAGCCATGACGCG 346
QY 272 tgattgcgtttgaaggaacgcgcgaatcgagtttgaaacgtacgcacctgaagcgc 328
DB 347 AGGTACACAGCTGGTACTACAACTTACATGATAGACGCGCTACAGACCCATAGCAC 403

RESULT 37
AA614629/c
LOCUS
DEFINITION
np54b11.s1 NCI_CGAP.Br1.1 Homo sapiens cDNA clone IMAGE:1130109 3' similar to gb:J04456 GALECTIN-1 (HUMAN);, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 505)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
Cloning Distribution: Washington University Genome Sequencing Center
Cloning Distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/IML at: www.bio.lnlnl.gov/bbrp/image/image.html
Insert Length: 549 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 388.
Location/Qualifiers
1..505
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1130109"
/clone_lib="NCI_CGAP.Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from pooled bulk breast tumor tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. (The normalized version of this library is NCI_CGAP.Br2.) Library was constructed by Bento Soares and M. Fatima Bonaldo."

FEATURES
source

AQ161443
 AQ161443.1 GI:3557844
 GSS.
 Magnaporthe grisea.
 Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 1 (bases 1 to 612)
 Yu, Y., Zhu, H., Boyd, C.A., Gaudette, B., Gayle, A., Kingsbury, R.,
 Phillips, K., Sasinowski, M., Wing, R.A. and Dean, R.A.
 A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
 Genome

REFERENCES

1 (bases 1 to 779)

1 (bases 1 to 779)

•